

IMMUNEX CORPORATION

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56
ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG	104					
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu						
1 5 10 15						
CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC	152					
Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr						
20 25 30						
TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG	200					
Phe Ser His Ser Pro Ile Ser Asn Phe Lys Val Lys Phe Arg Glu						
35 40 45						
TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT	248					
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn						
50 55 60						
CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC	296					
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala						
65 70 75 80						
CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA	344					
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln						
85 90 95						
ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT	392					
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys						
100 105 110						
ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC	440					
Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile						
115 120 125						

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TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC	488
Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro	
130 135 140	
TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG	536
Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln	
145 150 155 160	
TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC	584
Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala	
165 170 175	
CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC	632
Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu	
180 185 190	
CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG	680
Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp	
195 200 205	
GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG	728
Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly	
210 215 220	
GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA TCGTTGACTC	779
Val Pro Leu Pro Ser His Pro	
225 230	
AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT	839
TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC	879

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu	
1 5 10 15	
Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr	
20 25 30	
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu	
35 40 45	
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn	
50 55 60	
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala	
65 70 75 80	

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Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln
				85					90					95	
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys
			100					105					110		
Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile
		115					120					125			
Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro
	130					135						140			
Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln
145					150					155					160
Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala
				165					170					175	
Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu
			180					185					190		
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp
		195					200					205			
Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly
	210					215					220				
Val	Pro	Leu	Pro	Ser	His	Pro									
225					230										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG	485
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg	
140 145 150	
TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA	533
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro	
155 160 165	
TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC	581
Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro	
170 175 180	
CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC	629
Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala	
185 190 195 200	
GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC	677
Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg	
205 210 215	
CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT	725
Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu	
220 225 230	
GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC	774
Val Glu His	
235	
GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG	834
GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC	894
CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC	954
GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG	988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu	
1 5 10 15	
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe	
20 25 30	
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu	
35 40 45	
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu	
50 55 60	

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Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	65	70	75	80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	85	90	95	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	100	105	110	
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	115	120	125	
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	130	135	140	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	145	150	155	160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	165	170	175	
Thr	Ala	Pro	Thr	Ala	Pro	Gln	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	180	185	190	
Pro	Val	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Trp	Cys	Leu	His	Trp	Gln	195	200	205	
Arg	Thr	Arg	Arg	Arg	Thr	Pro	Arg	Pro	Gly	Glu	Gln	Val	Pro	Pro	Val	210	215	220	
Pro	Ser	Pro	Gln	Asp	Leu	Leu	Leu	Val	Glu	His						225	230	235	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC	TTTGGATAAA	AGAGACTACA	AGGACGACGA	TGACAAGACA	CCTGACTGTT	60
ACTTCAGCCA	C					71

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (ix) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (x) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
- (xi) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56										
ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	AGC	CCA	AAT	TCC	TCC	CTG	TTG	CTG	104
Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	
1				5					10					15		
CTG	TTG	CTG	CTG	CTG	AGT	CCT	TGC	CTG	CGG	GGG	ACA	CCT	GAC	TGT	TAC	152
Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	
				20				25					30			
TTC	AGC	CAC	AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA	GAG	200
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	
		35					40					45				
TTG	ACT	GAC	CAC	CTG	CTT	AAA	GAT	TAC	CCA	GTC	ACT	GTG	GCC	GTC	AAT	248
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	
	50					55					60					
CTT	CAG	GAC	GAG	AAG	CAC	TGC	AAG	GCC	TTG	TGG	AGC	CTC	TTC	CTA	GCC	296
Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	
65					70				75						80	
CAG	CGC	TGG	ATA	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	TCT	AAG	ATG	CAA	344
Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
				85					90					95		
ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	ATA	CAT	TTT	GTC	ACC	TCA	TGT	392
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	
			100					105					110			
ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	440
Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	
		115					120					125				
TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	CTT	GCT	CTG	AAG	CCC	488
Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro	
	130					135					140					

TGT	ATC	GGG	AAG	GCC	TGC	CAG	AAT	TTC	TCT	CGG	TGC	CTG	GAG	GTG	CAG	536
Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln	
145					150					155					160	
TGC	CAG	CCG	GAC	TCC	TCC	ACC	CTG	CTG	CCC	CCA	AGG	AGT	CCC	ATA	GCC	584
Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala	
				165					170					175		
CTA	GAA	GCC	ACG	GAG	CTC	CCA	GAG	CCT	CGG	CCC	AGG	CAG	CTG	TTG	CTC	632
Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu	
			180					185					190			
CTG	CTG	CTG	CTG	CTG	CCT	CTC	ACA	CTG	GTG	CTG	CTG	GCA	GCC	GCC	TGG	680
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp	
			195				200					205				
GGC	CTT	CGC	TGG	CAA	AGG	GCA	AGA	AGG	AGG	GGG	GAG	CTC	CAC	CCT	GGG	728
Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly	
	210					215					220					
GTG	CCC	CTC	CCC	TCC	CAT	CCC	TAGGATT	TCGA	GCCTTGTGCA	TCGTTGACTC						779
Val	Pro	Leu	Pro	Ser	His	Pro										
225					230											
AGCCAGGGTC	TTATCTCGGT	TACACCTGTA	ATCTCAGCCC	TTGGGAGCCC	AGAGCAGGAT											839
TGCTGAATGG	TCTGGAGCAG	GTCGTCTCGT	TCCAGTCGAC													879

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	
1				5					10					15		
Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	
			20					25					30			
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	
		35					40					45				
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	
	50					55					60					
Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	
65					70				75						80	
Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
			85						90					95		
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	
			100					105					110			

Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile
		115					120					125			
Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro
		130				135					140				
Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln
	145				150					155					160
Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala
				165					170					175	
Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu
			180					185					190		
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp
		195					200					205			
Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly
	210					215					220				
Val	Pro	Leu	Pro	Ser	His	Pro									
225					230										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT	TCCGGGGCCC	CCGGCCGAA	ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG		53				
			Met	Thr	Val	Leu	Ala	Pro	Ala	Trp						
			1				5									
AGC	CCA	ACA	ACC	TAT	CTC	CTC	CTG	CTG	CTG	CTG	AGC	TCG	GGA	CTC	101	
Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu		
	10					15				20						
AGT	GGG	ACC	CAG	GAC	TGC	TCC	TTC	CAA	CAC	AGC	CCC	ATC	TCC	TCC	GAC	149
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	
	25				30					35					40	
TTC	GCT	GTC	AAA	ATC	CGT	GAG	CTG	TCT	GAC	TAC	CTG	CTT	CAA	GAT	TAC	197
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	
				45					50					55		
CCA	GTC	ACC	GTG	GCC	TCC	AAC	CTG	CAG	GAC	GAG	GAG	CTC	TGC	GGG	GGC	245
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	
			60					65					70			
CTC	TGG	CGG	CTG	GTC	CTG	GCA	CAG	CGC	TGG	ATG	GAG	CGG	CTC	AAG	ACT	293
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	
		75					80					85				
GTC	GCT	GGG	TCC	AAG	ATG	CAA	GGC	TTG	CTG	GAG	CGC	GTG	AAC	ACG	GAG	341
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	
	90					95					100					
ATA	CAC	TTT	GTC	ACC	AAA	TGT	GCC	TTT	CAG	CCC	CCC	CCC	AGC	TGT	CTT	389
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	
105					110					115					120	
CGC	TTC	GTC	CAG	ACC	AAC	ATC	TCC	CGC	CTC	CTG	CAG	GAG	ACC	TCC	GAG	437
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	
				125					130					135		
CAG	CTG	GTG	GCG	CTG	AAG	CCC	TGG	ATC	ACT	CGC	CAG	AAC	TTC	TCC	CGG	485
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	
			140					145					150			
TGC	CTG	GAG	CTG	CAG	TGT	CAG	CCC	GAC	TCC	TCA	ACC	CTG	CCA	CCC	CCA	533
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	
		155					160						165			

TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
 170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
 Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
 185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
 205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC 774
 Val Glu His
 235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110

Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	
		115					120					125				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	
	130					135					140					
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	
145					150					155					160	
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	
				165					170					175		
Thr	Ala	Pro	Thr	Ala	Pro	Gln	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
			180					185					190			
Pro	Val	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Trp	Cys	Leu	His	Trp	Gln	
		195					200					205				
Arg	Thr	Arg	Arg	Arg	Thr	Pro	Arg	Pro	Gly	Glu	Gln	Val	Pro	Pro	Val	
	210					215					220					
Pro	Ser	Pro	Gln	Asp	Leu	Leu	Leu	Val	Glu	His						
225					230					235						

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT	60
ACTTCAGCCA C	71

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

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